



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 105277-1011

TO: Phillip Gambel
Location: CM1/8B03/9E12
Art Unit: 1644
Wednesday, October 08, 2003

Case Serial Number: 09/454651

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Gambel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib

115367

From: STIC-ILL
Sent: Monday, October 06, 2003 6:39 AM
To: STIC-Biotech/ChemLib
Subject: FW: 09 / 454651 ifw amd

-----Original Message-----

From: Gambel, Phillip
Sent: Saturday, October 04, 2003 9:43 AM
To: STIC-ILL
Subject: 09 / 454651 ifw amd

stic

please perform a sequence and a sequence interference search for

09 / 454,651 (ifw amd b7)

in PAPER

SEQ ID NO: 23

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 10/9/03
Date Completed: 10/8/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: Q2
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 10:45:40 ; Search time 67 seconds

(without alignments)
510.060 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVIVHTKEYKEVA.....LRVNTQFNWNTTKQHFPPD 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	226	10	US-09-915-789A-21
2	1149	100.0	288	8	US-08-592-711-2
3	1149	100.0	288	9	US-09-772-102-14
4	1149	100.0	288	9	US-09-837-867A-19
5	1149	100.0	288	10	US-09-910-174A-5
6	1149	100.0	288	10	US-09-896-738-10
7	1149	100.0	288	10	US-09-915-789A-15
8	1149	100.0	288	11	US-09-962-969-19
9	1149	100.0	288	11	US-09-350-202-2
10	1149	100.0	288	12	US-10-032-214-278
11	1149	100.0	288	12	US-10-126-088-2
12	1149	100.0	288	12	US-10-041-319-7
13	1149	100.0	288	13	US-10-261-101-2
14	1149	100.0	473	10	US-09-910-059-131
15	1143	99.5	492	10	US-09-845-899A-3

16	1129	98.3	288	12	US-10-032-214-94	Sequence 94, Appl
17	1121	97.6	288	12	US-10-032-214-69	Sequence 69, Appl
18	1121	97.6	288	12	US-10-032-214-82	Sequence 82, Appl
19	1119	97.4	288	12	US-10-032-214-71	Sequence 71, Appl
20	1119	97.4	288	12	US-10-032-214-77	Sequence 77, Appl
21	1119	97.4	288	12	US-10-032-214-225	Sequence 225, Appl
22	1118	97.3	288	12	US-10-032-214-84	Sequence 84, Appl
23	1116	97.1	288	12	US-10-032-214-76	Sequence 76, Appl
24	1116	97.1	288	12	US-10-032-214-85	Sequence 86, Appl
25	1116	97.1	288	12	US-10-032-214-87	Sequence 87, Appl
26	1116	97.1	288	12	US-10-032-214-286	Sequence 286, Appl
27	1114	97.0	288	12	US-10-032-214-236	Sequence 226, Appl
28	1114	97.0	288	12	US-10-032-214-251	Sequence 251, Appl
29	1113	96.9	288	12	US-10-032-214-90	Sequence 90, Appl
30	1113	96.9	288	12	US-10-032-214-228	Sequence 228, Appl
31	1113	96.9	288	12	US-10-032-214-250	Sequence 250, Appl
32	1112	96.8	288	12	US-10-032-214-78	Sequence 78, Appl
33	1112	96.8	288	12	US-10-032-214-248	Sequence 248, Appl
34	1111	96.7	288	12	US-10-032-214-238	Sequence 238, Appl
35	1110	96.6	288	12	US-10-032-214-236	Sequence 236, Appl
36	1110	96.5	288	12	US-10-032-214-88	Sequence 88, Appl
37	1109	96.5	288	12	US-10-032-214-89	Sequence 89, Appl
38	1109	96.5	288	12	US-10-032-214-92	Sequence 92, Appl
39	1109	96.5	288	12	US-10-032-214-249	Sequence 249, Appl
40	1108	96.4	287	12	US-10-032-214-243	Sequence 243, Appl
41	1105	96.2	288	12	US-10-032-214-81	Sequence 81, Appl
42	1104	96.1	287	12	US-10-032-214-74	Sequence 74, Appl
43	1104	96.1	300	12	US-10-032-214-232	Sequence 232, Appl
44	1103	96.0	288	12	US-10-032-214-91	Sequence 91, Appl
45	1103	96.0	288	12	US-10-032-214-229	Sequence 229, Appl

ALIGNMENTS

RESULT 1
US-09-915-789A-21
; Sequence 21, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match 100.0%; Score 1149; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 6.3e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIVHTKEYKEVATLSCGHNVSVVEELAQTRIYVQKEKRWLTMMSGDMNIWPE 60
DB 11 GLSHFCSGVIVHTKEYKEVATLSCGHNVSVVEELAQTRIYVQKEKRWLTMMSGDMNIWPE 70
QY 61 YKNTIFDITNNLSIVILALRPSDECTYECVVLKYEKDAFKREHLAEVTLVSKADFTPTS 120
DB 71 YKNTIFDITNNLSIVILALRPSDECTYECVVLKYEKDAFKREHLAEVTLVSKADFTPTS 130
QY 121 ISDFEPTSNIRRIICSTSGGFPPEPHLSWLENCEELNAINTVSQDPETELYAVSSKLD 180
DB 131 ISDFEPTSNIRRIICSTSGGFPPEPHLSWLENCEELNAINTVSQDPETELYAVSSKLD 190
QY 181 NMTTNHFMCLIKYGLHVRVNTQFNWNTTKQHFPPD 216

Db 191 NMTNHSFMCILKYGLRVNQTWNMTTKQEHFPDN 226
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US-08-592-711-2
RESULT 2
Sequence 2, Application US/08592711
Publication No. US20020115214A1
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/964,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE: for CD28 T cell surface antigen; transmembrane protein
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
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FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
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FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
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FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
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FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
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FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.

AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-592-711-2

Query Match 100.0%; Score 1149; DB 8; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVLELAQTRIYWKQKKWVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSODPETELYAVSSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSODPETELYAVSSKLDF 206
QY 181 NMTTNHSPMCLIKYGHRLRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTTNHSPMCLIKYGHRLRVNQTFFNNTTKQEHFPDN 242

RESULT 3

US-09-772-102-14
Sequence 14, Application US/09772102
Patent No. US20020006413A1
GENERAL INFORMATION:
APPLICANT: Sobol, Robert, E.
APPLICANT: Shawler, Daniel L.
APPLICANT: Bartholomew, Richard M.
APPLICANT: Carlo, Dennis J.
APPLICANT: Gold, Daniel P.
TITLE OF INVENTION: Genetically Engineered Tumor Cell
FILE REFERENCE: P-SO 4581
CURRENT APPLICATION NUMBER: US/09/772,102
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/178,498
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 288
TYPE: PRT
ORGANISM: Homo sapiens
US-09-772-102-14

Query Match 100.0%; Score 1149; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 146

QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSODPETELYAVSSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSODPETELYAVSSKLDF 206
QY 181 NMTTNHSPMCLIKYGHRLRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTTNHSPMCLIKYGHRLRVNQTFFNNTTKQEHFPDN 242

RESULT 4
US-09-837-867A-19
Sequence 19, Application US/09837867A
Patent No. US20020098542A1
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Bortello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
FILE REFERENCE: BWI-120CPADY
CURRENT APPLICATION NUMBER: US/09/837,867A
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 08/205,697
PRIOR FILING DATE: 1994-03-02
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 288
TYPE: PRT
ORGANISM: Homo sapiens
US-09-837-867A-19

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Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVLELAQTRIYWKQKKWVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSODPETELYAVSSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSODPETELYAVSSKLDF 206
QY 181 NMTTNHSPMCLIKYGHRLRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTTNHSPMCLIKYGHRLRVNQTFFNNTTKQEHFPDN 242

RESULT 5

US-09-910-174A-5
Sequence 5, Application US/09910174A
Patent No. US20020106730A1
GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730A1el Members of the B7
FILE REFERENCE: 35800/236924
CURRENT APPLICATION NUMBER: US/09/910,174A
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows version 4.0
SEQ ID NO 5
LENGTH: 288

Query Match 100.0%; Score 1149; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVLELAQTRIYWKQKKWVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 146

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174A-5

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Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCCLKYGHRLVNOTFNNTTKOEHPDN 216
DB 207 NMTNHSFMCCLKYGHRLVNOTFNNTTKOEHPDN 242

RESULT 6
US-09-896-738-10
; Sequence 10, Application US/09896738
; Patent No. US2002016347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Fang, Mei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 00-513-A
; CURRENT APPLICATION NUMBER: US/09/896,738
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 60/215,645
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-738-10

Query Match      100.0%; Score 1149; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCCLKYGHRLVNOTFNNTTKOEHPDN 216
DB 207 NMTNHSFMCCLKYGHRLVNOTFNNTTKOEHPDN 242

RESULT 7
US-09-915-789A-15
; Sequence 15, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
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; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-15

Query Match      100.0%; Score 1149; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCCLKYGHRLVNOTFNNTTKOEHPDN 216
DB 207 NMTNHSFMCCLKYGHRLVNOTFNNTTKOEHPDN 242

RESULT 8
us-09-962-969-19
; Sequence 19, Application US/09962969
; Publication No. US20030045703A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; Borriello, Francescopaolo
; Freeman, Gordon
; Nadler, Lee
; TITLE OF INVENTION: No. US20030045703A1el Forms of T Cell Costimulatory
; Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,969
; FILING DATE: 24-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/702,525
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
```

TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-962-969-19

Query Match 100.08: Score 1149: DB 11: Length 288:
 Best Local Similarity 100.08: Pred. No. 8.e-103:
 Matches 216: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 GLSHFCSGVHVTKEVATLSGCHNVSEELAQTRIVWQKKMYLTMMSSDMMIWP 60
 Db |
 27 GLSHFCSGVHVTKEVATLSGCHNVSEELAQTRIVWQKKMYLTMMSSDMMIWP 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVLYKADAFKREHLAEVTLVSKADFTPTS 120
 Db |
 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVLYKADAFKREHLAEVTLVSKADFTPTS 146
 QY 121 ISDFEIPSTNRRICSTSGGFPPEHLSWLENGEELNINTVSDPETELVAVSSKLD 180
 Db |
 147 ISDFEIPSTNRRICSTSGGFPPEHLSWLENGEELNINTVSDPETELVAVSSKLD 206
 QY 181 NMTNHSFMCILIKYGHVNVNFTNNNTTKEHFPDN 216
 Db |
 207 NMTNHSFMCILIKYGHVNVNFTNNNTTKEHFPDN 242

RESULT 9

US-09-350-202-2
 Sequence 2, Application US/09350202
 Publication No. US20030099643A1
 GENERAL INFORMATION:
 APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
 APPLICANT: Gray, Gary S., Rennett, Paul D.
 TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/350,202
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/403,253
 FILING DATE: March 10, 1995
 APPLICATION NUMBER: US 08/253,964
 FILING DATE: 3 JUNE 1994
 APPLICATION NUMBER: US 08/073,223
 FILING DATE: 4 JUNE 1993
 APPLICATION NUMBER: US 08/200,947
 FILING DATE: 23 FEB 1994
 APPLICATION NUMBER: US 07/864,805
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 08/247,505
 FILING DATE: 23 MAY 1994
 APPLICATION NUMBER: US 07/864,866
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 08/218,155
 FILING DATE: 25 MAR 1994

APPLICATION NUMBER: US 07/864,807
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 07/902,467
 FILING DATE: 16 JUNE 1992
 APPLICATION NUMBER: US 07/275,433
 FILING DATE: 23 NOV 1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: RPI-002CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: B cell activation antigen; natural ligand
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
 FEATURE:
 NAME/KEY: signal sequence
 LOCATION: -34 to -1
 IDENTIFICATION METHOD: amino terminal sequencing of
 IDENTIFICATION METHOD: soluble protein
 OTHER INFORMATION: hydrophobic
 FEATURE:
 NAME/KEY: extracellular domain
 LOCATION: 1 to 208
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: transmembrane domain
 LOCATION: 209 to 235
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: intracellular domain
 LOCATION: 236 to 254
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 19 to 21
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 55 to 57
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 64 to 66
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 152 to 154
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 173 to 175
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 177 to 179
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:

NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEDMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE W.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-350-202-2

Query Match 100.0%; Score 1149; DB 11; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVHVTKVEKVAITLSCGHNVSVEELAQTRIVYQKQKMYLTMSGDMNIWPE 60
DB 27 GLSHFCSGVHVTKVEKVAITLSCGHNVSVEELAQTRIVYQKQKMYLTMSGDMNIWPE 86
QY 61 YKNTIFDIINLSIVILALRPSDECTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDIINLSIVILALRPSDECTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRICTSGGFPPEHLWLENGEELNAINTVSQDPETELYAVSSKLDLF 180
DB 147 ISDFEPTSNIRRICTSGGFPPEHLWLENGEELNAINTVSQDPETELYAVSSKLDLF 206
QY 181 NMTNHSFMCLIKYGLRVNQTENNNTTKQEHFPDN 216
DB 207 NMTNHSFMCLIKYGLRVNQTENNNTTKQEHFPDN 242

RESULT 10
US-10-032-214-278
Sequence 278, Application US/10032214
Publication No. US20030138881A1
GENERAL INFORMATION:
APPLICANT: PUNNONEN, JUHA
APPLICANT: LAZETIC, ALEXANDRA
APPLICANT: LEONG, STEVEN R.
APPLICANT: CHANG, CHIA-CHUN
APPLICANT: APT, DORIS
APPLICANT: GUSTAFSSON, CLAES
TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
FILE REFERENCE: 02-106730US
CURRENT APPLICATION NUMBER: US/10/032.214
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 09/888,324

PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: PCT/US01/19973
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,946
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/241,245
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 320
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 278
LENGTH: 288
TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-214-278
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVHVTKVEKVAITLSCGHNVSVEELAQTRIVYQKQKMYLTMSGDMNIWPE 60
DB 27 GLSHFCSGVHVTKVEKVAITLSCGHNVSVEELAQTRIVYQKQKMYLTMSGDMNIWPE 86
QY 61 YKNTIFDIINLSIVILALRPSDECTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDIINLSIVILALRPSDECTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRICTSGGFPPEHLWLENGEELNAINTVSQDPETELYAVSSKLDLF 180
DB 147 ISDFEPTSNIRRICTSGGFPPEHLWLENGEELNAINTVSQDPETELYAVSSKLDLF 206
QY 181 NMTNHSFMCLIKYGLRVNQTENNNTTKQEHFPDN 216
DB 207 NMTNHSFMCLIKYGLRVNQTENNNTTKQEHFPDN 242

RESULT 11
US-10-126-088-2
Sequence 2, Application US/10126088
Publication No. US20030170821A1
GENERAL INFORMATION:
APPLICANT: FREEDMAN, GORDON J.
NADLER, LEE W.
TITLE OF INVENTION: DNA Encoding B7, A New Member
Of The Ig Superfamily With Unique Expression On
Activated And Neoplastic B Cells.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Dana-Farber Cancer Institute
STREET: 44 Binney Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM personal system 2; Model 30
OPERATING SYSTEM: MS/DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/126,088
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991
APPLICATION NUMBER: US 07/591,300
FILING DATE: 01-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: Ig V-set domain

LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J., FREEDMAN, ARNOLD S., SEGIL, JEFFREY M., LEE, GRACE, WHITMAN, JAMES F., NADLER, LEE M.,
TITLE: B7, A New Member Of the Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUFS IN SEQ ID NO: 2: From -26 to 262
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-126-088-2
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 216; Conservative 0;
Qy 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIVWQEKKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIVWQEKKKMVLTMMSGDMNIWPE 86
Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEPTSNIRRICSTSGFPPEHLSWLENELNAINTTVSQDPETELVAVSSKIDF 180
Db 147 ISDFEPTSNIRRICSTSGFPPEHLSWLENELNAINTTVSQDPETELVAVSSKIDF 206
Qy 181 NMTNHSFMCLIKYGHRLVRVNTQTNWNTTKQEHFPDN 216
Db 207 NMTNHSFMCLIKYGHRLVRVNTQTNWNTTKQEHFPDN 242
RESULT 12
US-10-041-319-7
; Sequence 7, Application US/10041319
; Publication No. US20030180309A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Baum, Peter R.
; APPLICANT: DuBose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HUMAN B7 POLYPEPTIDES
; FILE REFERENCE: 3176-A
; CURRENT APPLICATION NUMBER: US/10/041.319
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-319-7
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 216; Conservative 0;
Qy 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIVWQEKKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIVWQEKKKMVLTMMSGDMNIWPE 86

QY 61 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLKSWLENGEELNAINTVSQDPETELVAVSSKLD 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLKSWLENGEELNAINTVSQDPETELVAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLHVRVNTNNTTQOEHPDN 216
DB 207 NMTNHSFMCILIKYGLHVRVNTNNTTQOEHPDN 242

RESULT 13

US-10-261-101-2
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; Baskar, Sivasubramanian
; Glimcher, Laurie H.
; Freeman, Gordon J.
; Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/261.101
; FILING DATE: 30-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/966.148
; FILING DATE: 27-Sep-2000
; APPLICATION NUMBER: 08/147.772
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-261-101-2

Query Match 100.0%; Score 1149; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQKKEKVMVLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQKKEKVMVLTMMSGDMNIWPE 86
QY 61 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLKSWLENGEELNAINTVSQDPETELVAVSSKLD 180

DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLKSWLENGEELNAINTVSQDPETELVAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLHVRVNTNNTTQOEHPDN 216
DB 207 NMTNHSFMCILIKYGLHVRVNTNNTTQOEHPDN 242
RESULT 14
US-09-910-059-131
; Sequence 131, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910.059
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 09/171.945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
US-09-910-059-131

Query Match 100.0%; Score 1149; DB 10; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.7e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQKKEKVMVLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQKKEKVMVLTMMSGDMNIWPE 86
QY 61 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLKSWLENGEELNAINTVSQDPETELVAVSSKLD 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLKSWLENGEELNAINTVSQDPETELVAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLHVRVNTNNTTQOEHPDN 216
DB 207 NMTNHSFMCILIKYGLHVRVNTNNTTQOEHPDN 242

RESULT 15

US-09-845-899A-3
; Sequence 3, Application US/09845899A
; Patent No. US20020147326A1
; GENERAL INFORMATION:
; APPLICANT: CHAIKIN, MARGERY ANN
; APPLICANT: LYN, SALLY DOREEN PATRICIA
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMESEGED
; TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: P50496
; CURRENT APPLICATION NUMBER: US/09/845.899A

; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/202,346
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/043,948
; PRIOR FILING DATE: 1997-02-19
; PRIOR APPLICATION NUMBER: US 60/038,915
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 492
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-845-899A-3

Query Match 99.5%; Score 1143; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 6.9e-102;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVDELAAQTRIYWQEKKKVLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVDELAAQTRIYWQEKKKVLTMMSGDMNIWPE 80
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVSKADFTPS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVSKADFTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVSDPETELYAVSSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVSDPETELYAVSSKLDF 206
QY 181 NMTNHSEFMCLIKYGHRLRVNOTFNWNTTKOEHPD 215
DB 207 NMTNHSEFMCLIKYGHRLRVNOTFNWNTTKOEHPD 241

Search completed: October 7, 2003, 10:55:28
Job time : 68 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 10:33:15 ; Search time 23 seconds

(without alignments)
441.642 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149

Sequence: 1 GLSHFCGVIHVTKEVKA.....LRVNOTFNWTTKQEHFDPN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	1 CD80_HUMAN	P33681 oryctolagus
2	738	64.2	299	1 CD80_RABIT	P42070 mus musculus
3	561	48.8	306	1 CD80_MOUSE	Q00609 mus musculus
4	182	15.8	329	1 CD86_HUMAN	P42081 homo sapien
5	161	14.0	302	1 ICOL_HUMAN	O75144 homo sapien
6	152	13.2	309	1 CD86_MOUSE	P42082 mus musculus
7	150.5	13.1	322	1 ICOL_MOUSE	Q93b18 mus musculus
8	140.5	12.2	330	1 CD86_RABIT	P42071 oryctolagus
9	138	12.0	509	1 SHS1_RAT	P97710 r protein-t
10	134.5	11.7	583	1 C166_MOUSE	Q61490 mus musculus
11	133.5	11.6	583	1 C166_HUMAN	Q13740 homo sapien
12	129	11.2	221	1 BRFL_EBV	P03228 Epstein-bar
13	127	11.1	526	1 BUTY_HUMAN	Q13410 homo sapien
14	122.5	10.7	588	1 C166_CHICK	P42292 gallus gall
15	120.5	10.5	513	1 SHS1_MOUSE	P97797 m protein-t
16	120	10.4	506	1 SHS1_BOVIN	O46631 bos taurus
17	119	10.4	524	1 BUTY_MOUSE	Q62556 mus musculus
18	116.5	10.1	1088	1 NCAL_XENLA	P16170 xenopus lae
19	115	10.0	761	1 NCAL_HUMAN	P13592 homo sapien
20	115	10.0	848	1 NCAL_HUMAN	P13591 homo sapien
21	110.5	9.6	321	1 TCRB_FLY	P11364 feline leuk
22	110	9.6	398	1 SRB1_HUMAN	Q00241 homo sapien
23	109.5	9.5	646	1 MUI18_HUMAN	P43121 homo sapien
24	109.5	9.5	853	1 NCAL_BOVIN	P31836 bos taurus
25	109	9.5	387	1 SRB2_HUMAN	Q91w48 homo sapien
26	109	9.5	526	1 BUTY_BOVIN	P18892 bos taurus
27	109	9.5	2029	1 LAR_DROME	P16621 drosophila
28	108.5	9.4	365	1 CXAR_MOUSE	P97792 mus musculus
29	107.5	9.4	333	1 AMAL_DROME	P15364 drosophila
30	106.5	9.3	858	1 NCAL_RAT	P13596 rattus norv
31	105	9.1	319	1 A33_HUMAN	Q99795 homo sapien
32	105	9.1	1091	1 NCAL_CHICK	P13590 gallus gall
33	104	9.1	1092	1 NCAL_XENLA	P36335 xenopus lae

34	103.5	9.0	725	1	NCA2_MOUSE	P13594 mus musculus
35	103.5	9.0	1115	1	NCAL_MOUSE	P13595 mus musculus
36	103	9.0	298	1	JAM2_HUMAN	P57087 homo sapien
37	102.5	8.9	503	1	SHS1_HUMAN	P78324 h protein-t
38	102	8.9	1443	1	NEOL_CHICK	Q90610 gallus gall
39	101.5	8.8	403	1	RAGE_MOUSE	Q62151 mus musculus
40	100	8.7	413	1	HEMO_MANSE	P31398 manduca soc
41	99.5	8.7	1338	1	VGRI_HUMAN	P71948 h vascular
42	98.5	8.6	365	1	CXAR_HUMAN	P78310 homo sapien
43	98.5	8.6	1242	1	NPHN_MOUSE	Q9qz57 mus musculus
44	98	8.5	278	1	OX2G_RAT	P04218 rattus norv
45	98	8.5	298	1	JAM1_BOVIN	Q9xt56 bos taurus

ALIGNMENTS

RESULT :
CD80_HUMAN
1D CD80_HUMAN STANDARD: PRT; 288 AA.
AC P33681;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BBI).
GN CD80 OR CD28LG1 OR CD28LG OR LAB7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F., Nadler L.M.;
RA Nadler L.M.;
RT "B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells."
RL J. Immunol. 143:2714-2722(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307753; PubMed=1377173;
RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.;
RT "Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7."
RL Immunogenetics 36:175-181(1992).
RN [3]
RP SEQUENCE OF 35-38.
RX MEDLINE=91341422; PubMed=1714935;
RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7."
RL J. Exp. Med. 174:625-631(1991).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=95088403; PubMed=7527824;
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL."
RL J. Immunol. 154:97-105(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RX MEDLINE=20125021; PubMed=10661405;
RA Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K., Jones E.Y., Stuart D.I., Davis S.J.;
RT "Structure and dimerization of a soluble form of B7-1."
RL Immunity 12:51-60(2000).
CC !- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE

FT- TURN	156
STRAND	157
FT STRAND	171
FT STRAND	181
FT STRAND	186
FT STRAND	191
TURN	195
FT STRAND	198
FT STRAND	207
FT STRAND	208
FT STRAND	212
FT STRAND	221
FT STRAND	225
SQ SEQUENCE	288 AA; 33048 MW; BA453EE3A528B1F4 CRC64;

Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLSHPCSGVHVTKVEKVEATLSGCHNVSVEELAQTRIYWKOKKKWVLTHMNSGDMNTWPE	60
DB	27	GLSHPCSGVHVTKVEKVEATLSGCHNVSVEELAQTRIYWKOKKKWVLTHMNSGDMNTWPE	86
QY	61	YKNRTIEDITNNLSIVILALRPSDECTGYECVVLYKEKDFAFKREHLAEVTLTSVKADFPPTS	120
DB	87	YKNRTIEDITNNLSIVILALRPSDECTGYECVVLYKEKDFAFKREHLAEVTLTSVKADFPPTS	146
QY	121	ISDSEIPTSNIIRTCISGGPPEPHSLWNGEELNAINTTVSDDPETELYAVSSKLDF	180
DB	147	ISDSEIPTSNIIRTCISGGPPEPHSLWNGEELNAINTTVSDDPETELYAVSSKLDF	206
QY	181	NMTNHSPMCILIKYGLRLRVNOTFNWNTTKOEHPDN	216
DB	207	NMTNHSPMCILIKYGLRLRVNOTFNWNTTKOEHPDN	242

RESULT 2

ID	CD80_RABIT	STANDARD:	PRT: 299 AA.
AC	P42070;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen).		
DE	Cd80.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=B/J X CHBB;HM;		
RX	MEDLINE=95369849; PubMed=7642234;		
RA	Isono T., Seta A.;		
RT	"Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules.";		
RL	Immunogenetics 42:217-220(1995).		
CC	-!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. I CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.		
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL: D49843; BAA08643.1;		
DR			

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OM protein - protein search, using sw model

Run on: October 7, 2003, 10:40:10 ; Search time 96 Seconds

(without alignments)
580.618 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFGSGVHVTKEVKEVA.....LRVNTQFNWNTTKQBEHFDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phase:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-rvirus:*
- 16: sp-bacteriap:*
- 17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	97.3	288	6	077684
2	1100	95.7	288	6	Q28499
3	1085	94.4	288	6	Q9BDN6
4	1085	94.4	289	6	Q28347
5	772	67.2	296	6	Q8WM22
6	764	66.5	230	6	Q9N213
7	762.5	66.4	288	6	Q9TT70
8	762.5	66.4	297	6	Q9BE99
9	761	66.2	229	6	Q9TT71
10	743	64.7	292	6	Q9GM28
11	743	64.7	292	6	Q02758
12	719	62.6	304	6	Q9IQX1
13	717.5	62.4	296	6	Q46405
14	705	61.4	235	6	Q9N070
15	705	61.4	235	6	Q9TQ58
16	659	57.4	294	11	Q8BH36

17	603.5	52.5	321	11	035187
18	602	52.4	290	11	Q62680
19	601.5	52.3	321	11	Q62624
20	596	51.9	321	11	055202
21	560	48.7	306	11	09R129
22	350	30.5	174	6	Q9GM29
23	349.5	30.4	173	6	Q9SL17
24	255.5	22.2	212	11	061332
25	200.5	17.4	329	6	Q9XSX6
26	200.5	17.4	332	6	Q9GM27
27	200.5	17.4	332	6	Q9SL16
28	188.5	16.4	280	6	Q9TTF1
29	188.5	16.4	296	13	042404
30	182	15.8	329	6	Q9TTF2
31	178	15.5	323	6	Q9BDN2
32	177	15.4	323	6	Q9BDN9
33	177	15.4	323	6	Q9BDM4
34	176	15.3	275	6	Q9BDN9
35	176	15.3	323	6	Q9BDN8
36	171	14.9	284	6	Q9GL33
37	166.5	14.5	289	11	08K3J3
38	165	14.4	281	11	08CJE8
39	162	14.1	313	11	035531
40	161.5	14.1	325	6	002838
41	159	13.8	316	11	08V598
42	156.5	13.6	290	4	Q9NZ07
43	153	13.3	290	11	Q9EP73
44	153	13.3	356	11	064381
45	152	13.2	314	11	061238

ALIGNMENTS

RESULT 1

077684 ID 077684 PRELIMINARY; PRT; 288 AA.
AC 077684;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE B7 protein.
GN B7.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1];
RP SEQUENCE FROM N.A.
RA Kraus G., Hnatyszyn J.H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079519; AAC31555.1;
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
SQ SEQUENCE 288 AA; 33131 MW; 76BRC42839F9AR79 CRC64;

Query Match 97.3%; Score 1118; DB 6; Length 288;
Best Local Similarity 97.7%; Pred. No. 1e-92;
Matches 210; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LSHFGSGVHVTKEVKEVATLSCGHNVSVEELATRIYVQKEKKWLTMMSCDMNWP 61
DB 28 LSHFGSGVHVTKEVKEVATLSCGHNVSVEELATRIYVQKEKKWLTMMSCDMNWP 87
QY 62 NRTFTDITNLISVILALRPSDEGIVKVEKDAFKREHLAEVTLVSKADFTPS 121
DB 88 NRTFTDITNLISVILALRPSDEGIVKVEKDAFKREHLAEVTLVSKADFTPS 147

QY 122 SDFEIPSTNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELAVSSKLDNF 181
 DB 148 TDFEIPSPNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGHVRVNOTFNWNTTKOEHPDN 216
 DB 208 MTNHSFMCILIKYGHVRVNOTFNWNTTKOEHPDN 242

RESULT 2

Q28499 ID Q28499 PRELIMINARY: PRT: 288 AA.
 AC Q28499
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE B7 protein (CD80 protein precursor).
 GN B7 OR N939.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 0:0-0(2001).
 DR EMBL: U19840; AAK86706.1; -;
 DR EMBL: AF344849; AAK37609.1; -;
 DR HSSP: P33681; IDR9.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; IG_1.
 DR PROSITE: PS50835; IG-LIKE; 2.
 KW Signal.
 FT SIGNAL 1 26 POTENTIAL.
 SQ SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match 95.7%; Score 1100; DB 6; Length 288;
 Best Local Similarity 96.3%; Pred. No. 4.2e-91;
 Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKVLTMSGDMNIWPEY 61
 DB 28 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKVLTMSGDMNIWPEY 87
 QY 62 KNRTIFDTNNLSIVILALRPSDEGYECVLYKEDAFKREHLAEVTLVKADFTPSI 121
 DB 88 KNRTIFDTNNLSIVILALRPSDEGYECVLYKEDAFKREHLAEVTLVKADFTPSI 147
 QY 122 SDFEIPSTNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELAVSSKLDNF 181
 DB 148 TDFEIPSPNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGHVRVNOTFNWNTTKOEHPDN 216
 DB 208 MTNHSFMCILIKYGHVRVNOTFNWNTTKOEHPDN 242

RESULT 3

Q9BDN6 ID Q9BDN6 PRELIMINARY: PRT: 288 AA.
 AC Q9BDN6
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE CD80 protein.
 GN MNB71.
 OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Cercocebus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344839; AAK37535.1; -;
 DR HSSP: P33681; IDR9.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; IG_1.
 DR PROSITE: PS50835; IG-LIKE; 1.
 SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;

Best Local Similarity 95.3%; Pred. No. 9.4e-90;

Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKVLTMSGDMNIWPEY 61
 DB 28 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKVLTMSGDMNIWPEY 87
 QY 62 KNRTIFDTNNLSIVILALRPSDEGYECVLYKEDAFKREHLAEVTLVKADFTPSI 121
 DB 88 KNRTIFDTNNLSIVILALRPSDEGYECVLYKEDAFKREHLAEVTLVKADFTPSI 147
 QY 122 SDFEIPSTNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELAVSSKLDNF 181
 DB 148 TDFEIPSPNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGHVRVNOTFNWNTTKOEHPDN 216
 DB 208 MTNHSFMCILIKYGHVRVNOTFNWNTTKOEHPDN 242

RESULT 4

Q28347 ID Q28347 PRELIMINARY: PRT: 289 AA.
 AC Q28347
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE B7 protein (Fragment).
 GN B7.
 OS Cercocebus torquatus (red-crowned mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Cercocebus.
 OX NCBI_TaxID=9530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and